

AMENDMENT TO THE CLAIMS

1. (*Currently amended*) A program storage device accessible by a computer,
5 tangible embodying a program of instructions executable by said computer
 to perform method steps for protein structure alignment, ~~said methods~~
 steps comprising of:
- (a) means for receiving atomic coordinates of a first protein with N_1 atoms;
 - (b) means for receiving atomic coordinates of a second protein with N_2 atoms;
 - 10 (c) means for making an initial alignment of said atoms of said first protein to
 said atoms of said second protein;
 - (d) means for calculating all atomic distances between said atomic
 coordinates of said atoms of said first protein and said atomic coordinates
 of said atoms of said second protein;
 - 15 (e) means for defining a matrix with a plurality of binary assignment variables
 wherein each binary assignment variable corresponding to either a match
 or to a gap;
 - (f) means for defining one or more mean field equations wherein said
 plurality of binary assignment variables are replaced by a plurality of
20 continuous mean field variables, whereby said each mean field variable
 has a value between 0 and 1, and a plurality of forces that are proportional
 to said atomic distances squared;
 - (g) means for formulating an energy function, wherein:
 said energy function includes a first cost for each said atomic distance
25 wherein said distance is a weighted body transformation using said
 continuous mean field variables of said first protein while keeping said
 second protein fixed; ,
 said energy function includes a second cost λ for each said gap by either
 said first protein or said second protein,
30 said energy function includes a third cost δ for a position-independent
 consecutive said gap; ,

said energy function includes a fourth cost for enforcing a constraint to satisfy that each said atom of said first protein either aligns with said atom of said second protein or to said gap;

- (h) means for minimizing by an iterative process of said energy function and updating said continuous mean field variables in said mean field equations for a decreasing set of temperatures T until convergence to a predefined convergence value is reached; and
- (i) means for after convergence rounding off said continuous mean field variables to either 0 or 1.

2. (*Currently amended*) The program storage device method as set forth in claim 1, wherein said means for ~~step of~~ formulating an energy function further comprises a fifth cost for discouraging crossed matches.

3. (*Currently amended*) The program storage device method as set forth in claim 1, wherein said second cost λ is a value between 0.01 and 0.5.

4. (*Currently amended*) The program storage device method as set forth in claim 3, wherein said second cost λ for a α -site in a α -helix has a larger said second cost λ by a factor between 0.01 and 0.5 of said second cost λ .

5. (*Currently amended*) The program storage device method as set forth in claim 3, wherein said second cost λ for a β -sheet has a larger said second cost λ by a factor between 0.01 and 0.5 of said second cost λ .

6. (*Currently amended*) The program storage device method as set forth in claim 1, wherein said third cost δ is a function of said second cost λ divided by a value between 1 and 20.

7. (*Currently amended*) The program storage device method as set forth in claim 1, wherein fourth cost includes a parameter γ with a value between 0 and 0.2.
- 5 8. (*Currently amended*) The program storage device method as set forth in claim 1, wherein said means for step of minimizing by an iterative process includes an iteration parameter ϵ with a value between 0.5 and 0.95.
- 10 9. (*Currently amended*) The program storage device method as set forth in claim 1, wherein said means for step of minimizing by an iterative process further comprises the step of initiating said temperature to a value between 1 and 100.
- 15 10. (*Currently amended*) A method of using a mean field approach for protein structure alignment, comprising the steps of:
- (a) providing receiving atomic coordinates of a first protein with N_1 atoms;
 - (b) providing receiving atomic coordinates of a second protein with N_2 atoms;
 - (c) making an initial alignment of said atoms of said first protein to said atoms
20 of said second protein;
 - (d) calculating all atomic distances between said atomic coordinates of said atoms of said first protein and said atomic coordinates of said atoms of said second protein;
 - (e) defining a matrix with a plurality of binary assignment variables wherein
25 each binary assignment variable corresponding to either a match or to a gap;
 - (f) defining one or more mean field equations wherein said plurality of binary assignment variables are replaced by a plurality of continuous mean field variables, whereby said each mean field variable has a value between 0 and 1, and a plurality of forces that are proportional to said atomic distances
30 squared;
 - (g) formulating an energy function, wherein:

said energy function includes a first cost for each said atomic distance wherein said distance is a weighted body transformation using said continuous mean field variables of said first protein while keeping said second protein fixed; ,

5 said energy function includes a second cost λ for each said gap by either said first protein or said second protein,

said energy function includes a third cost δ for a position-independent consecutive said gap; ,

10 said energy function includes a fourth cost for enforcing a constraint to satisfy that each said atom of said first protein either aligns with said atom of said second protein or to said gap;

(h) minimizing by an iterative process of said energy function and updating said continuous mean field variables in said mean field equations for a decreasing set of temperatures T until convergence to a predefined convergence value is reached; and

15 (i) after convergence rounding off said continuous mean field variables to either 0 or 1.

20 11. (*Original*) The method as set forth in claim 10, wherein said step of formulating an energy function further comprises a fifth cost for discouraging crossed matches.

25 12. (*Original*) The method as set forth in claim 10, wherein said second cost λ is a value between 0.01 and 0.5.

13. (*Original*) The method as set forth in claim 12, wherein said second cost λ for a α -site in a α -helix has a larger said second cost λ by a factor between 0.01 and 0.5 of said second cost λ .

14. (*Original*) The method as set forth in claim 12, wherein said second cost λ for a β -sheet has a larger said second cost λ by a factor between 0.01 and 0.5 of said second cost λ .
- 5 15. (*Original*) The method as set forth in claim 10, wherein said third cost δ is a function of said second cost λ divided by a value between 1 and 20.
- 10 16. (*Original*) The method as set forth in claim 10, wherein fourth cost includes a parameter γ with a value between 0 and 0.2.
- 15 17. (*Original*) The method as set forth in claim 10, wherein said step of minimizing by an iterative process includes an iteration parameter ϵ with a value between 0.5 and 0.95.
18. (*Original*) The method as set forth in claim 10, wherein said step of minimizing by an iterative process further comprises the step of initiating said temperature to a value between 1 and 100.